

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SAMPATH, K. T.

COHEN, C.

EIICHI, O.

KOHEI, M.

KAWABATA, M.

(ii) TITLE OF INVENTION: METHODS FOR MAINTAINING OR RESTORING TISSUE-APPROPRIATE PHENOTYPE OF SOFT TISSUE CELLS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

(B) STREET: 45 SOUTH STREET

(C) CITY: HOPKINTON

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 01748

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CAMACHO, JENNIFER A.

(B) REGISTRATION NUMBER: P-43,526

(C) REFERENCE/DOCKET NUMBER: CRP-160

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)-248-7000

(B) TELEFAX: (617)-248-7100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1067 base pairs

(B) TYPE: nucleic acid

09581770.122900

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..1067

(D) OTHER INFORMATION: /product= "MOUSE TYPE 10 COLLAGEN
PROMOTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCGATCCTAA AACACTTAAG GATATTTCTG TAAGGCTGTG AAAGAGAAAA CCAACTACTT 60
ACACGGATGG AGACCATGTT TATTCTTTG GGAGAAAAGC CTAATTGGGA CGCTTCGAGA 120
TCCCTATAGG AAATTGCACC AGTAGTCAAC TGGATTTTAA AAAGGCAAAG CTTGAGGATT 180
TTTTTTTCCC TTGAAATGA ATGTAGCAAA CTTATGTAAG CACGGAATAG GATTATTAGT 240
TAACAGTCTT TTCAATTATA TGGGAAAATG AAAACTAGGG GAGCGTCTAA GGCCACTTGC 300
TGACCTTTGT GCAGCTGTTA AGTAAAGAAA GTAAACCCTC CAGGGATACT GAACAGCCAA 360
CTGTCATAAG TCCAGGTGT CTTGCACTTG CTGTGACAAG TTAAAATAT TTAATATGAC 420
TATACCTGAA ATATTTAATG CTATCTTTT CATGCACCAG CTTCTAAGAG CTTTCCCTAA 480
AATCCTGATA TGCAAAGAA TATACCAATA TTTTCCCCCT TGCCCCTGGC GCTTGTCTCC 540
CAAGTTAGCA AACACTTAGG TAAGCGATTT TTACAGAACT TTTTCCCTA ATAACTGAAG 600
GACTAACATG ATGATTAGA TCTATATTCT CCCCAAAGG CGTCTCATAT TTTGTATAT 660
TACCAAATAT TTTAGTCAA ATAACACAAG AATGTATTTT AAAAATAAAA AGGGTGAATC 720
ATCATTCCAT CATGAACCAA CATTGGACTC AGAACTCCTA AAAGGAAAAC AGAAAAAAAA 780
AAAAAATCAT GCACAGCCGA AGCTATTAAT ATATAATGGA GACAAAGAGT TTATTTTCA 840
ATGAGAATAA CAAGGAAAAA AGCCTGATT TGTACGCCTG CCCGTTAGGA CTTCCCACCA 900
TAATTAGTGC TTCTGCCCC TGAGAGGAGG AGCTTCGGCT CAGGGGAACT TCATGCAATA 960
AGGAAGAAA ACAGTATAAA TACTCCAGGG CAGCCGTGGG GAAGGCATTA TCCACTGCTC 1020

006227 02278560

CTGGGCAGAG GAAGCCAGGA AAGCTGCCCC ACGCATCTCC CAGCACC

1067

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "AP1 SEQUENCE A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGCTTGATGA CTCAGCCGGA A

21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /product= "AP1 SEQUENCE A MUTATION"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCTCATCA

10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid

006221"0228560

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "Conserved domain of human c-fos"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Val Glu Gln Leu Ser Pro Glu Glu Glu Lys Arg Arg Ile Arg
1 5 10 15

Arg Ile Arg Asn Lys Met Ala Ala Ala
20 25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= "AP-1 CONSENSUS SEQUENCE B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACTCAGC GCGGA

15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /product= "MEF-2 CONSENSUS"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAAAAATAA C

11

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1341
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "OP1"
/evidence= EXPERIMENTAL
/standard_name= "OP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG
Met His Val

57

1

CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala

105

09581770 122900

5 10 15

CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC 153
 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
 20 25 30 35

GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG 201
 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
 40 45 50

CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC 249
 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
 55 60 65

CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG 297
 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
 70 75 80

CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC 345
 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
 85 90 95

GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC 393
 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
 100 105 110 115

CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC 441
 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
 120 125 130

ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC 489
 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
 135 140 145

CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC 537
 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
 150 155 160

CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC 585
 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
 165 170 175

TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT 633
 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
 180 185 190 195

CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC 681
 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
 200 205 210

005221 0778560

GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC 729
 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
 215 220 225

ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG 777
 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
 230 235 240

GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC 825
 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
 245 250 255

AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC 873
 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
 260 265 270 275

TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC 921
 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
 280 285 290

CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC 969
 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
 295 300 305

AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC 1017
 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
 310 315 320

AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC 1065
 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
 325 330 335

CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC 1113
 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
 340 345 350 355

GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG 1161
 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
 360 365 370

AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC 1209
 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
 375 380 385

CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC 1257
 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
 390 395 400

006221 0478560

ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA 1305
Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
405 410 415

TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC 1351
Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
420 425 430

GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGCCAG 1411

GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG 1471

TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC 1531

ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC 1591

GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651

CGTTTCCAGA GGTAATTATG AGCGCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711

GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771

CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

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